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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/028,384

DATE: 01/16/2002  
TIME: 14:42:42

Input Set A:\es.txt  
Output Set N:\CRF3\01162002\J028384.raw

ENTERED

3 <110> APPLICANT: COMPATIGENE INC.  
4 PERREAULT, Claude  
5 MCBRIDE, Kevin  
7 <120> TITLE OF INVENTION: Mammalian SIMP, gene sequence and uses thereof in cancer  
therapy  
9 <130> FILE REFERENCE: 5600-74  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/028,384  
C--> 11 <141> CURRENT FILING DATE: 2001-12-20  
11 <160> NUMBER OF SEQ ID NOS: 13  
13 <170> SOFTWARE: PatentIn version 3.1  
15 <210> SEQ ID NO: 1  
16 <211> LENGTH: 2481  
17 <212> TYPE: DNA  
18 <213> ORGANISM: Homo sapiens  
20 <220> FEATURE  
21 <221> NAME/KEY: CDS  
32 <222> LOCATION: (1)..(2481)  
23 <223> OTHER INFORMATION  
26 <400> SEQUENCE 1  
27 atg gcg gaa ccc tcc gcc ccg gag agc aag cac aag tcg tcc ctc aac 48  
28 Met Ala Glu Pro Ser Ala Pro Glu Ser Lys His Lys Ser Ser Leu Asn  
29 1 5 10 15  
31 tcg tcc ccg tgg agt ggc ctc atg gcc ctg gga aac aac agc ccg cac ggc 96  
32 Ser Ser Pro Trp Ser Gly Leu Met Ala Leu Gly Asn Ser Arg His Gly  
33 20 25 30  
35 cac cac ggg ccc ggg gcc cag tgc gcg cac aag gcg gcg ggc ggc 144  
36 His His Gly Pro Gly Ala Gln Cys Ala His Lys Ala Ala Gly Gly Ala  
37 35 40 45  
39 gcg ccg ccg aag ccg gcc ccg gcg ggg ctg tcc ggg ggg ctg tcg cag 192  
40 Ala Pro Pro Lys Pro Ala Pro Ala Gly Leu Ser Gly Gly Leu Ser Gln  
41 50 55 60  
43 ccg gct ggg tgg cag tcg ctt ctc tcc acc atc ctc ttc ctg gcc 240  
44 Pro Ala Gly Trp Gln Ser Leu Leu Ser Phe Thr Ile Leu Phe Leu Ala  
45 65 70 75 80  
47 tgg ctt gcc ggc ttc agc tcg cgc ctc ttc gcc gtc atc cgc ttc gaa 288  
48 Trp Leu Ala Gly Phe Ser Ser Arg Leu Phe Ala Val Ile Arg Phe Glu  
49 85 90 95  
51 agc atc atc cac gag ttc gac ccg tgg ttt aac tat aga tca aca cat 336  
52 Ser Ile Ile His Glu Phe Asp Pro Trp Phe Asn Tyr Arg Ser Thr His  
53 100 105 110  
55 cat ctt gca tct cat ggg ttc tat gaa ttt tta aat tgg ttt gat gaa 384  
56 His Leu Ala Ser His Gly Phe Tyr Glu Phe Leu Asn Trp Phe Asp Glu  
57 115 120 125  
59 aga gca tgg tat cca cta gga aga ata gta ggt ggt act gtt tac cca 432  
60 Arg Ala Trp Tyr Pro Leu Gly Arg Ile Val Gly Gly Thr Val Tyr Pro  
61 130 135 140  
63 ggg ttg atg ata acc gct ggc ctt att cat tgg att tta aat aca ttg 480  
64 Gly Leu Met Ile Thr Ala Gly Leu Ile His Trp Ile Leu Asn Thr Leu

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65	145	150	155	160															
67	aac	ata	act	gtt	cac	ata	aga	gac	gta	tgt	gtg	ttc	ctt	gca	cca	act	528		
68	Asn	Ile	Thr	Val	His	Ile	Arg	Asp	Val	Cys	Val	Phe	Leu	Ala	Pro	Thr			
69																165	170	175	
71	ttt	agc	gac	ctt	aca	tct	ata	tct	act	ttc	ctg	ctt	aca	aga	gaa	ctt	576		
72	Phe	Ser	Gly	Leu	Thr	Ser	Ile	Ser	Thr	Phe	Leu	Leu	Thr	Arg	Glu	Leu			
73																180	185	190	
75	tgg	aac	caa	gga	gca	gga	ctt	tta	gtc	gtc	tgt	ttt	att	gtc	att	gta	624		
76	Trp	Asn	Gln	Gly	Ala	Gly	Leu	Leu	Ala	Ala	Cys	Phe	Ile	Ala	Ile	Val			
77																195	200	205	
79	cca	ggc	tar	ata	tct	cg	tc	gta	gtc	gja	tcc	ttt	gat	aat	gaa	gjc	672		
80	Pro	Gly	Tyr	Ile	Ser	Arg	Ser	Val	Ala	Gly	Ser	Phe	Asp	Asn	Glu	Gly			
81																210	215	220	
83	att	gtc	att	ttt	gca	ctt	cag	ttc	aca	tac	tat	tta	tgg	gta	aaa	tct	720		
84	Ile	Ala	Ile	Phe	Ala	Leu	Gln	Phe	Thr	Tyr	Tyr	Leu	Trp	Val	Lys	Ser			
85																225	230	235	240
87	gta	aaa	act	ggg	tca	gtt	ttt	tgg	aca	atg	tgc	tgc	tgc	tta	tcc	tat	768		
88	Val	Lys	Thr	Gly	Ser	Val	Phe	Trp	Thr	Met	Cys	Cys	Cys	Leu	Ser	Tyr			
89																245	250	255	
91	ttc	tat	atg	gtc	tct	gtc	tct	gtt	ggt	ggt	tat	gta	ttt	atc	atc	aat	ctt	816	
92	Phe	Tyr	Met	Val	Ser	Ala	Trp	Gly	Gly	Tyr	Val	Phe	Ile	Ile	Asn	Leu			
93																260	265	270	
95	att	cca	ctg	cat	gta	ttt	gtg	ttg	tta	ctg	atg	cag	aga	tac	agc	aaa	864		
96	Ile	Pro	Leu	His	Val	Phe	Val	Leu	Leu	Leu	Met	Gln	Arg	Tyr	Ser	Lys			
97																275	280	285	
99	aga	gtc	tac	ata	gca	tat	agc	act	ttc	tac	att	gtg	ggt	tta	ata	tta	912		
100	Arg	Val	Tyr	Ile	Ala	Tyr	Ser	Thr	Phe	Tyr	Ile	Val	Gly	Leu	Ile	Leu			
101																290	295	300	
103	tca	atg	cag	ata	cct	ttt	gtg	gga	ttc	cag	cca	atc	aga	aca	agt	gaa	960		
104	Ser	Met	Gln	Ile	Pro	Phe	Val	Gly	Phe	Gln	Pro	Ile	Arg	Thr	Ser	Glu			
105																305	310	315	320
107	cac	atg	gca	gtc	gca	ggt	gtc	ttt	gca	ttg	ctg	caa	gtc	tat	gtc	ttc	1008		
108	His	Met	Ala	Ala	Ala	Gly	Val	Ala	Leu	Leu	Met	Gln	Ala	Tyr	Ala	Phe			
109																325	330	335	
111	ttg	cag	tat	ctg	aga	gac	cga	tta	aca	aaa	caa	gag	ttc	cag	acc	ctt	1056		
112	Leu	Gln	Tyr	Leu	Arg	Asp	Arg	Leu	Thr	Lys	Gln	Glu	Phe	Gln	Thr	Leu			
113																340	345	350	
115	ttc	ttt	ttg	ggt	gta	tca	cta	gtc	gca	ggt	gtc	gtc	ttt	ctt	agt	gtc	1104		
116	Phe	Phe	Leu	Gly	Val	Ser	Leu	Ala	Ala	Gly	Ala	Val	Phe	Leu	Ser	Val			
117																355	360	365	
119	atc	tat	ttg	act	tat	aca	ggt	tac	att	gca	cca	tgg	agt	ggc	agg	ttt	1152		
120	Ile	Tyr	Leu	Thr	Tyr	Thr	Gly	Tyr	Ile	Ala	Pro	Trp	Ser	Gly	Arg	Phe			
121																370	375	380	
123	tat	tca	ttg	tgg	gat	act	ggg	tat	gca	aaa	ata	cac	att	cca	att	att	1200		
124	Tyr	Ser	Leu	Trp	Asp	Thr	Gly	Tyr	Ala	Lys	Ile	His	Ile	Pro	Ile	Ile			
125																385	390	395	400
127	gca	tca	gtg	tct	gag	cat	caa	cct	acg	act	tgg	gtg	tct	ttc	ttc	ttt	1248		
128	Ala	Ser	Val	Ser	Glu	His	Gln	Pro	Thr	Thr	Trp	Val	Ser	Phe	Phe	Phe			
129																405	410	415	

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131	gat	cta	cat	att	ctt	gta	tgt	atc	ttc	cca	gca	ggc	ctt	tgg	ttc	tgc	1296
132	Asp	Leu	His	Ile	Leu	Val	Cys	Thr	Phe	Pro	Ala	Gly	Leu	Trp	Phe	Cys	
133				430											430		
135	atc	aaa	aat	atc	aaa	gat	gaa	aga	gta	ttt	gtt	gct	cta	tat	gca	atc	1344
136	Ile	Lys	Asn	Ile	Asn	Asp	Glu	Arg	Val	Phe	Val	Ala	Leu	Tyr	Ala	Ile	
137				435											445		
138	agt	gtc	taa	ttt	gtc	gga	gtg	atg	gtg	cja	ctt	atg	tgg	act	ttt		1392
140	Ser	Ala	Val	Tyr	Phe	Ala	Gly	Val	Met	Val	Arg	Leu	Met	Leu	Thr	Leu	
141				450											450		
143	act	cca	gtc	gtg	tgt	atg	ctg	tct	gca	att	gcc	ttt	tca	aat	gtt	ttt	1440
144	Thr	Pro	Val	Val	Cys	Met	Leu	Ser	Ala	Ile	Ala	Phe	Ser	Asn	Val	Phe	
145	455				470										480		
147	gag	caa	tat	ttt	ggg	gat	gac	atg	aaa	agg	gaa	aat	cca	cct	gtg	gag	1488
148	Glu	His	Tyr	Leu	Gly	Asp	Asp	Met	Lys	Arg	Glu	Asn	Pro	Pro	Val	Glu	
149				485											495		
151	gac	agc	agt	gat	gag	gat	gac	aaa	aga	aaa	caa	gaa	aat	tgg	tat	gat	1536
152	Asp	Ser	Ser	Asp	Glu	Asp	Asp	Lys	Arg	Asn	Gln	Gly	Asn	Leu	Tyr	Asp	
153				500											510		
155	aaq	gca	ggt	aaa	gtt	agg	aaa	cat	gca	act	gaa	cug	gaa	aaa	act	gaa	1584
156	Lys	Ala	Gly	Lys	Val	Arg	Lys	His	Ala	Thr	Glu	Gln	Glu	Lys	Thr	Glu	
157				515											525		
159	gag	gga	tta	ggc	ctt	aat	ata	aaa	agc	att	gtc	acc	atg	tgg	atg	ctg	1632
160	Glu	Gly	Leu	Gly	Pro	Asn	Ile	Lys	Ser	Ile	Val	Thr	Met	Leu	Met	Leu	
161				530											540		
163	atg	cta	tgg	atg	ttt	gtc	cac	tgt	acc	tgg	gtc	aca	agc	aat			1680
164	Met	Leu	Leu	Met	Phe	Ala	Val	His	Cys	Thr	Trp	Val	Thr	Ser	Asn		
165	545				550										560		
167	gcc	taa	tct	agt	cca	agt	gta	gtc	ctg	gcc	tca	tac	aat	cat	gat	ggc	1728
168	Ala	Tyr	Ser	Ser	Pro	Ser	Val	Val	Leu	Ala	Ser	Tyr	Asn	His	Asp	Gly	
169				565											575		
171	acc	agg	aat	atc	tta	gat	gat	ttt	aga	gaa	gtc	tac	ttt	tgg	cta	agg	1776
172	Thr	Arg	Asn	Ile	Leu	Asp	Asp	Phe	Arg	Glu	Ala	Tyr	Phe	Trp	Leu	Arg	
173				580											590		
175	caa	aat	aca	gat	gaa	cat	gca	cga	gta	atg	tct	tgg	tgg	gat	tat	ggc	1824
176	Gln	Asn	Thr	Asp	Gln	His	Ala	Arg	Val	Met	Ser	Trp	Trp	Asp	Tyr	Gly	
177				595											605		
179	tat	cag	ata	gtc	gga	atg	gtc	aat	aga	act	acg	tgg	gtg	gat	aat	aac	1872
180	Tyr	Gln	Ile	Ala	Gly	Met	Ala	Asn	Arg	Thr	Leu	Val	Asp	Asn	Asn		
181				610											620		
183	acc	tgg	aat	aac	agc	cac	ata	gca	ctg	gtg	gga	aaa	gct	atg	tct	tct	1920
184	Thr	Trp	Asn	Asn	Ser	His	Ile	Ala	Leu	Val	Gly	Lys	Ala	Met	Ser	Ser	
185	625				630										640		
187	aat	gaa	aca	gca	gcc	tat	aaa	atc	atg	agg	act	cta	gat	gta	gat	tat	1968
188	Asn	Glu	Thr	Ala	Ala	Tyr	Lys	Ile	Met	Arg	Thr	Leu	Asp	Val	Asp	Tyr	
189				645											655		
191	gtt	ttt	ttt	ttt	gga	ggg	gtt	att	ggc	tat	tct	ggt	gat	gat	atc		2016
192	Val	Leu	Val	Ile	Phe	Gly	Gly	Val	Ile	Gly	Tyr	Ser	Gly	Asp	Asp	Ile	
193				660											670		
195	aac	aaa	ttt	ctc	tgg	atg	gtt	agg	ata	gct	gaa	gga	caa	cat	ccc	aaa	2064

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196	Asn	Lys	Phe	Leu	Trp	Met	Val	Arg	Ile	Ala	Glu	Glu	His	Pro	Lys		
197						675				680					685		
198	gac	att	cgt	gaa	agt	gac	tat	ttt	acc	cca	cag	gga	gaa	ttc	cgt	gtt	2112
199	Asp																
200	Asp	Ile	Arg	Glu	Ser	Asp	Tyr	Phe	Thr	Pro	Gln	Gly	Glu	Phe	Arg	Val	
201						690			695					700			
202	gac	aaa	gca	gga	ttc	cct	act	ttt		2160							
203	Asp	Lys	Ala	Gly	Ser	Pro	Thr	Leu	Leu	Asn	Cys	Leu	Met	Tyr	Lys	Met	
204															710	715	
205																720	
206	tca	tac	tac	aga	ttt	gga	gaa	atg	cag	ctg	gtt	ttt	cgt	aca	ccc	cca	
207	Ser	Tyr	Tyr	Arg	Phe	Gly	Glu	Met	Gln	Leu	Asp	Phe	Arg	Thr	Pro	Pro	
208						725			730					735			
209	gtt	ttt	gac	cga	aca	cgt	aat	gtt	gag	att	gga	aat	aag	gac	att	aaa	
210	Gly	Phe	Asp	Arg	Thr	Arg	Asn	Ala	Glu	Ile	Gly	Asn	Lys	Asp	Ile	Lys	
211						740			745					750			
212	tcc	aaa	cac	ttt	gaa	gaa	gcc	ttt	aca	tca	gaa	cac	tgg	ttt	gtt	agg	
213	Phe	Lys	His	Leu	Glu	Glu	Ala	Phe	Thr	Ser	Glu	His	Trp	Leu	Val	Arg	
214						755			760					765			
215	ata	tat	aaa	gtt	aaa	gca	cct	gtt	aat	aac	agg	gag	aca	tta	gtt	cac	aaa
216	Ile	Tyr	Lys	Val	Lys	Ala	Pro	Asp	Asn	Arg	Glu	Thr	Leu	Asp	His	Lys	
217						770			775					780			
218	gtt	ttt	gca	acc	aac	att	ttt	cca	aaa	cag	aag	tat	ttt	ttt	ttt	ttt	2400
219	Pro	Arg	Val	Thr	Asn	Ile	Phe	Pro	Lys	Gln	Lys	Tyr	Leu	Ser	Lys		
220						785			790					795		800	
221	act	acc	aaa	agg	aag	cgt	ttt	2448									
222	Thr	Thr	Lys	Arg	Lys	Arg	Gly	Tyr	Ile	Lys	Asn	Lys	Leu	Val	Phe	Lys	
223						805			810					815			
224	aaa	tgc	aag	aaa	ata	tct	aag	aag	act	gtt	ttt	ttt	ttt	ttt	ttt	ttt	2481
225	Lys	Gly	Lys	Lys	Ile	Ser	Lys	Lys	Thr	Val							
226						820			825								
227	ttt	2481															
228	ttt																
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272	115	120	125	
275	Arg Ala Trp Tyr Pro Leu Gly Arg Ile Val Gly Gly Thr Val Tyr Pro			
276	130	135	140	
279	Gly Leu Met Ile Thr Ala Gly Leu Ile His Trp Ile Leu Asn Thr Leu			
280	145	150	155	160
283	Asn Ile Thr Val His Ile Arg Asp Val Cys Val Phe Leu Ala Pro Thr			
284	165	170	175	
287	Phe Ser Gly Leu Thr Ser Ile Ser Thr Phe Leu Leu Thr Arg Glu Leu			
288	180	185	190	
291	Trp Asn Gln Gly Ala Gly Leu Leu Ala Ala Cys Phe Ile Ala Ile Val			
292	195	200	205	
295	Pro Gly Tyr Ile Ser Arg Ser Val Ala Gly Ser Phe Asp Asn Glu Gly			
296	210	215	220	
299	Ile Ala Ile Phe Ala Leu Gln Phe Thr Tyr Tyr Leu Trp Val Lys Ser			
300	225	230	235	240
303	Val Lys Thr Gly Ser Val Phe Trp Thr Met Cys Cys Cys Leu Ser Tyr			
304	245	250	255	
307	Phe Tyr Met Val Ser Ala Trp Gly Gly Tyr Val Phe Ile Ile Asn Leu			
308	260	265	270	
311	Ile Pro Leu His Val Phe Val Leu Leu Leu Met Gln Arg Tyr Ser Lys			
312	275	280	285	
315	Arg Val Tyr Ile Ala Tyr Ser Thr Phe Tyr Ile Val Gly Leu Ile Leu			
316	290	295	300	
319	Ser Met Gln Ile Pro Phe Val Gly Phe Gln Pro Ile Arg Thr Ser Glu			
320	305	310	315	320
323	His Met Ala Ala Ala Gly Val Phe Ala Leu Leu Gln Ala Tyr Ala Phe			
324	325	330	335	
327	Leu Gln Tyr Leu Arg Asp Arg Leu Thr Lys Gln Glu Phe Gln Thr Leu			
328	340	345	350	
331	Phe Phe Leu Gly Val Ser Leu Ala Ala Gly Ala Val Phe Leu Ser Val			
332	355	360	365	
335	Ile Tyr Leu Thr Tyr Thr Gly Tyr Ile Ala Pro Trp Ser Gly Arg Phe			
336	370	375	380	
339	Tyr Ser Leu Trp Asp Thr Gly Tyr Ala Lys Ile His Ile Pro Ile Ile			
340	385	390	395	400
343	Ala Ser Val Ser Glu His Gln Pro Thr Thr Trp Val Ser Phe Phe			
344	405	410	415	
347	Asp Leu His Ile Leu Val Cys Thr Phe Pro Ala Gly Leu Trp Phe Cys			
348	420	425	430	
351	Ile Lys Asn Ile Asn Asp Glu Arg Val Phe Val Ala Leu Tyr Ala Ile			
352	435	440	445	
355	Ser Ala Val Tyr Phe Ala Gly Val Met Val Arg Leu Met Leu Thr Leu			
356	450	455	460	
359	Thr Pro Val Val Cys Met Leu Ser Ala Ile Ala Phe Ser Asn Val Phe			
360	465	470	475	480
363	Glu His Tyr Leu Gly Asp Asp Met Lys Arg Glu Asn Pro Pro Val Glu			
364	485	490	495	
367	Asp Ser Ser Asp Glu Asp Asp Lys Arg Asn Gln Gly Asn Leu Tyr Asp			
368	500	505	510	

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date